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RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/988,745

TIME: 18:58:12

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SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
      5
             (i) APPLICANT: LI, Yi and RUBEN, Steven
     7
            (ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR
           (iii) NUMBER OF SEQUENCES: 10
      9
            (iv) CORRESPONDENCE ADDRESS:
     ĨĨ
                  (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
     12
                  (B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
     13
                  (C) CITY: WASHINGTON
     14
     15
                  (D) STATE: DC
                  (E) COUNTRY: UNITED STATES OF AMERICA
     16
                                                                    ENTERED
     17
                  (F) ZIP: 20005-3934
             (V) COMPUTER READABLE FORM:
     19
                  (A) MEDIUM TYPE: Floppy disk
     20
                  (B) COMPUTER: IBM PC compatible
     21
     22
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     23
     25
            (vi) CURRENT APPLICATION DATA:
                  (A) APPLICATION NUMBER: US/09/988,745
C--> 26
C--> 27
                  (B) FILING DATE: 20-Nov-2001
     28
                  (C) CLASSIFICATION:
C--> 30
           (vii) PRIOR APPLICATION DATA:
     31
                  (A) APPLICATION NUMBER: 09/314,006
     32
                  (B) FILING DATE:
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                  (A) NAME: STEFFE, ERIC K
     36
                  (B) REGISTRATION NUMBER: 36,688
     37
                  (C) REFERENCE/DOCKET NUMBER: 1488.0840001
     39
            (ix) TELECOMMUNICATION INFORMATION:
     40
                  (A) TELEPHONE: (202) 371-2600
     41
                  (B) TELEFAX: (202) 371-2540
        (2) INFORMATION FOR SEQ ID NO: 1:
     46
             (i) SEQUENCE CHARACTERISTICS:
     47
                  (A) LENGTH: 1380 base pairs
     48
                  (B<sub>i</sub>) TYPE: nucleic acid
     49
                  (C') STRANDEDNESS: double
     50
                  (D) TOPOLOGY: linear
     52
            (ii) MOLECULE TYPE: DNA (genomic)
     55
            (ix) FEATURE:
     56
                  (A) NAME/KEY: CDS
     57
                  (B) LOCATION: 252..1262
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     62 CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGGAAAC CATTCTTCAA TTGAATTTCA
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     64 GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT
                                                                                 120
     66 CCTCCTCCTC GTTTCACCCT GTGAGTAATT AACAGACAAA ATTTTTTTTT TTTTTTTT
                                                                                 180
     68 TTTTTTTTT TTTTTGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT
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70 AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT

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Output Set: N:\CRF3\01152002\1988745.raw

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79 Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met 80 30 35 40 45 82 CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC 83 Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr 84 50 55 60 86 TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC CTG GCC 87 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala 88 65 70 75 90 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTC CTG AGC ACT 91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 92 80 85 90 94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TCC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC GCC CAC TGT GCC ATC TTC GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GTC CTC AGG TAC ATC CTC 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACC TCG TTA TTC CTC TGC CTC 107 GTG GTG GTG GTG CTC GTG GTG GTG GTG GTG
80 30 35 40 45 82 CTG ATT ATC GTG CTA GGG AAT GTA TT GTG GCA TTT GCT GTC TAC A34 82 CTG ATT ATC GTG CTA GGG AAT GTA TT GTG GCA TTT GCT GTC TAC A43 83 Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Sar Tyr 56 G0 66 71 CAC AAG GC CCC ACC AAC TTC CTG CTG CTC CTG GCC 75 GC 76 TTC AAA GCG CTC CAC ACG CCC ACC AAC TTC CTG CTG CTC CTC CTG GCC 75 CTG CTG GTG GAC ATG TTT CTG GGT CTG CTG GTG CTC TCC CTG GCC 75 CTG GTG GAC ATG TTT CTG GGT CTG CTG GTG CTC CTC AGC ACC ATT 75 CTG GAC ATG TTT CTG GGT CTG CTG GTG CTC CTC AGC ACC ATT 11 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 90 00 90 90 90 90 90 90 90 90 90 90 90
82 CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC 83 Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr 84 50 60 60 61 TC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC CTC CTG GCC 60 61 TC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC 60 61 TC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC 61 TAC ACC ATG TTT CTG GGT CTG CTG GTG CTC CTC CTG CTC AGC ACC ATT 61 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Leu Ala 62 80 63 85 64 TC CTA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 65 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 64 95 65 100 60 61 TAT CAT CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 626 63 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 646 65 100 61 10 62 115 62 120 63 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 646 65 100 674 675 674 675 676 677 678 678 679 679 679 670 670 670 670 670 670 670 670 670 670
83 Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr 84 50 55 60 86 TTC AAA GGG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC CTG GCC 482 87 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala 88 65 70 75 90 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTC CTC AGC ACC ATT 91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 92 80 85 90 94 CGC TCA GTG GAG AGC TGC TGT GTC TTC GGG GAC TTC CTG CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 100 100 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TCC CATC CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 100 126 127 TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GTC TC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC TCC TTA TTC CTG TAC ACC AGG TAC 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC TCC TTC TAC ACC AGG TAC 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGC GGA GAG ATC CTC TAC ACA GAT 116 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 117 14 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG GTG 118 GGC AGT TGC CAG CTG CTG AGT AGA TTT TGG GGC TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC GCC CTG CTC ATT ATG ATC AGC TTG TAT GTG AAG 120 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
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86 TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC CTC CTG GCC 87 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala 88 65 70 75 90 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CTC AGC ACC ATT 91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 92 80 85 90 94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACC TTC TAC TC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAC TGG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
87 Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Ser Leu Ala 88
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90 CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT 91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 92 80 85 90 94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC TG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG GCA GAA GAG ATG CCT TGT GTG 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG GCA GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTC CAT AAA TATT TG GG GCT TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
91 Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile 92 80 85 90 94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTC CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
92
94 CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG 95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TCC CTC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTG CTC CTC AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
95 Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu 96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Ann Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
96 95 100 105 98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110 115 120 125 102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104 130 135 140 106 TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA 107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 150 155 110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 770 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112 160 165 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116 175 180 185 118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914
98 CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC 99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110
99 His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu 100 110
100 110
102 TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC 103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104
103 Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu 104
104
107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 145 150 155 155 155 160 770 110 GGA TGG GGG GTG CCC GCA GCA ACT TCG TTA TTC CTC ACA GAT 770 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 170 170 170 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG AGC AGG CTG AGC CAG TGG CTG AGC AGG AGC AGC AGG AGC CAG TTG AGC A
107 Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala 108 145 145 150 155 155 155 160 770 110 GGA TGG GGG GTG CCC GCA GCA ACT TCG TTA TTC CTC ACA GAT 770 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 170 170 170 170 114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG AGC AGG CTG AGC CAG TGG CTG AGC AGG AGC AGC AGG AGC CAG TTG AGC A
110 GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT 111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112
111 Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp 112
112
114 GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116
115 Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val 116
116 175 180 185 118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 866 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 200 120 190 195 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
118 GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 119 Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
119 Gly Ser Cys Gln Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe 120 190
120 190 195 200 205 122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
122 CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
123 Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
144 ATJ 44V
126 ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC 962
127 Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser
128 225 230 235
130 AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC 1010
131 Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr
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Input Set : N:\Crf3\RULE60\09988745.raw
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154	TTG	TAC		GAA	TGA	rrcci	rTC 1		AATO	C AC	GCA	AGGAC		GAC	CTCA		1302
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156	Lou	335	02														
	CAGO		TAT A	AAGTO	GGCAG	CT G	rgaco	CGCGC	GC:	rgrg	rggt	GTTC	AGT	rrg :	rggg	CATGCT	1362
160																	1380
163						SEO	ID 1	10: 2	2:								
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172						ESCR:			SEQ :	D NO): 2	:					
174 1	Met												Pro	Ala	Ala	Phe	1
175	1	_			5					10					15		
177 (Cys	Tyr	Gln	Val	Asn	Gly	Ser	Cys	Pro	Arg	Thr	Val	His	Thr	Leu	Gly	
178									25					30			
100				20					23					30			
TOO .	Ile	Gln	Leu		Ile	Tyr	Leu	Thr		Ala	Ala	Gly	Met		Ile	Ile	
181	Ile	Gln	Leu 35		Ile	Tyr	Leu	Thr 40		Ala	Ala	Gly	Met 45		Ile	Ile	
			35	Val		_		40	Cys				45	Leu			
181			35	Val		_		40	Cys				45	Leu			
181 183 '	Val	Leu 50	35 Gly	Val Asn	Val	Phe	Val 55	40 Ala	Cys Phe	Ala	Val	Ser 60	45 Tyr	Leu Phe	Lys	Ala	
181 183 184 186 187	Val Leu 65	Leu 50 His	35 Gly Thr	Val Asn Pro	Val Thr	Phe Asn 70	Val 55 Phe	40 Ala Leu	Cys Phe Leu	Ala Leu	Val Ser 75	Ser 60 Leu	45 Tyr Ala	Leu Phe Leu	Lys Ala	Ala Asp 80	
181 183 184 186	Val Leu 65	Leu 50 His	35 Gly Thr	Val Asn Pro	Val Thr Leu	Phe Asn 70	Val 55 Phe	40 Ala Leu	Cys Phe Leu	Ala Leu Leu	Val Ser 75	Ser 60 Leu	45 Tyr Ala	Leu Phe Leu	Lys Ala Ser	Ala Asp 80	
181 183 184 186 187 189 1	Val Leu 65 Met	Leu 50 His Phe	35 Gly Thr Leu	Val Asn Pro Gly	Val Thr Leu 85	Phe Asn 70 Leu	Val 55 Phe Val	40 Ala Leu Leu	Cys Phe Leu Pro	Ala Leu Leu 90	Val Ser 75 Ser	Ser 60 Leu Thr	45 Tyr Ala Ile	Leu Phe Leu Arg	Lys Ala Ser 95	Ala Asp 80 Val	
181 183 184 186 187 189 190 192	Val Leu 65 Met	Leu 50 His Phe	35 Gly Thr Leu	Val Asn Pro Gly Trp	Val Thr Leu 85	Phe Asn 70 Leu	Val 55 Phe Val	40 Ala Leu Leu	Cys Phe Leu Pro Phe	Ala Leu Leu 90	Val Ser 75 Ser	Ser 60 Leu Thr	45 Tyr Ala Ile	Leu Phe Leu Arg	Lys Ala Ser 95	Ala Asp 80 Val	
181 183 184 186 187 189 190 192 193	Val Leu 65 Met Glu	Leu 50 His Phe Ser	35 Gly Thr Leu Cys	Val Asn Pro Gly Trp 100	Val Thr Leu 85 Phe	Phe Asn 70 Leu Phe	Val 55 Phe Val Gly	40 Ala Leu Leu Asp	Cys Phe Leu Pro Phe 105	Ala Leu Leu 90 Leu	Val Ser 75 Ser Cys	Ser 60 Leu Thr	45 Tyr Ala Ile Leu	Leu Phe Leu Arg His 110	Lys Ala Ser 95 Thr	Ala Asp 80 Val Tyr	
181 183 184 186 187 189 190 192 193 195	Val Leu 65 Met Glu	Leu 50 His Phe Ser	35 Gly Thr Leu Cys	Val Asn Pro Gly Trp 100	Val Thr Leu 85 Phe	Phe Asn 70 Leu Phe	Val 55 Phe Val Gly	40 Ala Leu Leu Asp	Cys Phe Leu Pro Phe 105	Ala Leu Leu 90 Leu	Val Ser 75 Ser Cys	Ser 60 Leu Thr	45 Tyr Ala Ile Leu Leu	Leu Phe Leu Arg His 110	Lys Ala Ser 95 Thr	Ala Asp 80 Val Tyr	
181 183 184 186 187 189 190 192 193 195 196	Val Leu 65 Met Glu Leu	Leu 50 His Phe Ser	35 Gly Thr Leu Cys Thr 115	Val Asn Pro Gly Trp 100 Leu	Val Thr Leu 85 Phe	Phe Asn 70 Leu Phe Cys	Val 55 Phe Val Gly Leu	40 Ala Leu Leu Asp Thr 120	Cys Phe Leu Pro Phe 105 Ser	Ala Leu Leu 90 Leu Ile	Val Ser 75 Ser Cys Phe	Ser 60 Leu Thr Arg	45 Tyr Ala Ile Leu Leu 125	Leu Phe Leu Arg His 110 Cys	Lys Ala Ser 95 Thr	Ala Asp 80 Val Tyr	
181 183 184 186 187 189 190 192 193 195 196 198	Val Leu 65 Met Glu Leu	Leu 50 His Phe Ser Asp	35 Gly Thr Leu Cys Thr 115	Val Asn Pro Gly Trp 100 Leu	Val Thr Leu 85 Phe	Phe Asn 70 Leu Phe Cys	Val 55 Phe Val Gly Leu Ala	40 Ala Leu Leu Asp Thr 120	Cys Phe Leu Pro Phe 105 Ser	Ala Leu Leu 90 Leu Ile	Val Ser 75 Ser Cys Phe	Ser 60 Leu Thr Arg His	45 Tyr Ala Ile Leu Leu 125	Leu Phe Leu Arg His 110 Cys	Lys Ala Ser 95 Thr	Ala Asp 80 Val Tyr	
181 183 184 186 187 189 190 192 193 195 196 198 199	Val Leu 65 Met Glu Leu Ser	Leu 50 His Phe Ser Asp Ile 130	35 Gly Thr Leu Cys Thr 115 Asp	Val Asn Pro Gly Trp 100 Leu Arg	Val Thr Leu 85 Phe Phe	Phe Asn 70 Leu Phe Cys	Val 55 Phe Val Gly Leu Ala 135	40 Ala Leu Leu Asp Thr 120 Ile	Cys Phe Leu Pro Phe 105 Ser Cys	Ala Leu 90 Leu Ile Asp	Val Ser 75 Ser Cys Phe	Ser 60 Leu Thr Arg His Leu 140	45 Tyr Ala Ile Leu Leu 125 Leu	Leu Phe Leu Arg His 110 Cys	Lys Ala Ser 95 Thr Phe	Ala Asp 80 Val Tyr Ile Ser	
181 183 184 186 187 189 190 192 193 195 196 198 199 201	Val Leu 65 Met Glu Leu Ser Lys	Leu 50 His Phe Ser Asp Ile 130	35 Gly Thr Leu Cys Thr 115 Asp	Val Asn Pro Gly Trp 100 Leu Arg	Val Thr Leu 85 Phe Phe	Phe Asn 70 Leu Phe Cys Val	Val 55 Phe Val Gly Leu Ala 135	40 Ala Leu Leu Asp Thr 120 Ile	Cys Phe Leu Pro Phe 105 Ser Cys	Ala Leu 90 Leu Ile Asp	Val Ser 75 Ser Cys Phe Pro Ile	Ser 60 Leu Thr Arg His Leu 140	45 Tyr Ala Ile Leu Leu 125 Leu	Leu Phe Leu Arg His 110 Cys	Lys Ala Ser 95 Thr Phe	Ala Asp 80 Val Tyr Ile Ser Gly	
181 183 184 186 187 189 190 192 193 195 196 198 199 201 202	Val Leu 65 Met Glu Leu Ser Lys 145	Leu 50 His Phe Ser Asp Ile 130 Phe	35 Gly Thr Leu Cys Thr 115 Asp	Val Asn Pro Gly Trp 100 Leu Arg Val	Val Thr Leu 85 Phe Phe His	Phe Asn 70 Leu Phe Cys Val 150	Val 55 Phe Val Gly Leu Ala 135 Ala	40 Ala Leu Leu Asp Thr 120 Ile Leu	Cys Phe Leu Pro Phe 105 Ser Cys Arg	Ala Leu 90 Leu Ile Asp	Val Ser 75 Ser Cys Phe Pro Ile 155	Ser 60 Leu Thr Arg His Leu 140 Leu	45 Tyr Ala Ile Leu Leu 125 Leu Ala	Leu Phe Leu Arg His 110 Cys Tyr Gly	Lys Ala Ser 95 Thr Phe Pro	Ala Asp 80 Val Tyr Ile Ser Gly 160	
181 183 184 186 187 189 190 192 193 195 196 198 199 201 202 204	Val Leu 65 Met Glu Leu Ser Lys 145	Leu 50 His Phe Ser Asp Ile 130 Phe	35 Gly Thr Leu Cys Thr 115 Asp	Val Asn Pro Gly Trp 100 Leu Arg Val	Val Thr Leu 85 Phe Phe His Arg	Phe Asn 70 Leu Phe Cys Val 150	Val 55 Phe Val Gly Leu Ala 135 Ala	40 Ala Leu Leu Asp Thr 120 Ile Leu	Cys Phe Leu Pro Phe 105 Ser Cys Arg	Ala Leu 90 Leu Ile Asp Tyr Leu	Val Ser 75 Ser Cys Phe Pro Ile 155	Ser 60 Leu Thr Arg His Leu 140 Leu	45 Tyr Ala Ile Leu Leu 125 Leu Ala	Leu Phe Leu Arg His 110 Cys Tyr Gly	Lys Ala Ser 95 Thr Phe Pro Trp Val	Ala Asp 80 Val Tyr Ile Ser Gly 160	
181 183 184 186 187 189 190 192 193 195 196 198 199 201 202 204 205	Val Leu 65 Met Glu Leu Ser Lys 145 Val	Leu 50 His Phe Ser Asp Ile 130 Phe Pro	35 Gly Thr Leu Cys Thr 115 Asp Thr	Asn Pro Gly Trp 100 Leu Arg Val	Val Thr Leu 85 Phe Phe His Arg Tyr 165	Phe Asn 70 Leu Phe Cys Val 150 Thr	Val 55 Phe Val Gly Leu Ala 135 Ala	40 Ala Leu Leu Asp Thr 120 Ile Leu	Cys Phe Leu Pro Phe 105 Ser Cys Arg Phe	Ala Leu 90 Leu Ile Asp Tyr Leu 170	Val Ser 75 Ser Cys Phe Pro Ile 155 Tyr	Ser 60 Leu Thr Arg His Leu 140 Leu	45 Tyr Ala Ile Leu 125 Leu Ala Asp	Leu Phe Leu Arg His 110 Cys Tyr Gly Val	Lys Ala Ser 95 Thr Phe Pro Trp Val 175	Ala Asp 80 Val Tyr Ile Ser Gly 160 Glu	
181 183 184 186 187 189 190 192 193 195 196 198 199 201 202 204	Val Leu 65 Met Glu Leu Ser Lys 145 Val	Leu 50 His Phe Ser Asp Ile 130 Phe Pro	35 Gly Thr Leu Cys Thr 115 Asp Thr	Asn Pro Gly Trp 100 Leu Arg Val	Val Thr Leu 85 Phe Phe His Arg Tyr 165	Phe Asn 70 Leu Phe Cys Val 150 Thr	Val 55 Phe Val Gly Leu Ala 135 Ala	40 Ala Leu Leu Asp Thr 120 Ile Leu	Cys Phe Leu Pro Phe 105 Ser Cys Arg Phe	Ala Leu 90 Leu Ile Asp Tyr Leu 170	Val Ser 75 Ser Cys Phe Pro Ile 155 Tyr	Ser 60 Leu Thr Arg His Leu 140 Leu	45 Tyr Ala Ile Leu 125 Leu Ala Asp	Leu Phe Leu Arg His 110 Cys Tyr Gly Val	Lys Ala Ser 95 Thr Phe Pro Trp Val 175	Ala Asp 80 Val Tyr Ile Ser Gly 160 Glu	



Input Set : N:\Crf3\RULE60\09988745.raw
Output Set: N:\CRF3\01152002\1988745.raw

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210 Gln Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe
                                200
            195
213 Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val
       210
                            215
                                                 220
216 Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu
                                             235
                        230
219 Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile
                                         250
                    245
222 Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr
223
                                    265
                260
225 Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp
            275
226
228 Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile
                                                 300
                            295
231 Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu
                                             315
232 305
                        310
234 Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln
                    325
                                         330
235
237 Glu
240 (2) INFORMATION FOR SEQ ID NO: 3:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 29 base pairs
243
              (B) TYPE: nucleic acid
244
              (C) STRANDEDNESS: single
245
              (D) TOPOLOGY: linear
246
        (ii) MOLECULE TYPE: DNA (genomic)
248
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
253
                                                                             29
255 CGGAATTCCT UATGAGAGCT GTCTTCATC
257 (2) INFORMATION FOR SEQ ID NO: 4:
        (i) SEQUENCE CHARACTERISTICS:
259
              (A) LENGTH: 32 base pairs
260
              (B) TYPE: nucleic acid
261
262
              (C) STRANDEDNESS: single
263
              (D) TOPOLOGY: linear
265
        (ii) MOLECULE TYPE: DNA (genomic)
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                              32
272 CGGAAGCTTC GTCATTCTTG GTACAAATCA AC
274 (2) INFORMATION FOR SEQ ID NO: 5:
276
         (i) SEQUENCE CHARACTERISTICS:
277
              (A) LENGTH: 30 base pairs
278
              (B) TYPE: nucleic acid
279
              (C) STRANDEDNESS: single
280
              (D) TOPOLOGY: linear
282
        (ii) MOLECULE TYPE: DNA (genomic)
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
287
                                                                             30
289 CGGGATCCCT CCATGAGAGC TGTCTTCATC
291 (2) INFORMATION FOR SEQ ID NO: 6:
293
        (i) SEQUENCE CHARACTERISTICS:
294
              (A) LENGTH: 29 base pairs
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Input Set: N:\Crf3\RULE60\09988745.raw
Output Set: N:\CRF3\01152002\1988745.raw

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(B) TYPE: nucleic acid
     295
                   (C) STRANDEDNESS: single
     296
     297
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: DNA (genomic)
     299
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     304
                                                                                   29
     306 CGGGATCCCG CTCATTCTTG GTACAAATC
     308 (2) INFORMATION FOR SEQ ID NO: 7:
              (i) SEQUENCE CHARACTERISTICS:
     310
                   (A) LENGTH: 34 base pairs
     311
     312
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: single
     313
                   (D) TOPOLOGY: linear
     314
             (ii) MOLECULE TYPE: DNA (genomic)
     316
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
     321
                                                                                   34
     323 GTCCAAGCTT GCCACCATGA GAGCTGTCTT CATC
     325 (2) INFORMATION FOR SEQ ID NO: 8:
     327
              (i) SEQUENCE CHARACTERISTICS:
     328
                   (A) LENGTH: 61 base pairs
     329
                   (B) TYPE: nucleic acid
     330
                   (C) STRANDEDNESS: single
                   (D) TOPOLOGY: linear
     331
             (ii) MOLECULE TYPE: DNA (genomic)
     333
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                   60
     340 CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCATTCTTGG TACAAATCAA
                                                                                   61
     342 C
     344 (2) INFORMATION FOR SEQ ID NO: 9:
              (i) SEQUENCE CHARACTERISTICS:
     347
                   (A) LENGTH: 365 amino acids
     348
                   (B) TYPE: amino acid
                   (C) STRANDEDNESS: Not Relevant
     349
W--> 350
                   (D) TOPOLOGY: Not Relevant
     352
             (ii) MOLECULE TYPE: protein
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
     357
              Ala Arg Leu Leu Val Leu Ala Ser Pro Pro Ala Ser Leu Leu Pro Pro
     359
     360
                               5
                                                    10
              Ala Ser Glu Gly Ser Ala Pro Leu Ser Gln Gln Trp Thr Ala Gly Met
     362
     363
                           20
                                                25
              Gly Leu Leu Val Ala Leu Ile Val Leu Leu Ile Val Val Gly Asn Val
     365
     366
     368
              Leu Val Ile Val Ala Ile Ala Lys Thr Pro Arg Leu Gln Thr Leu Thr
     369
                                       55
                                                            60
              Asn Leu Phe Ile Met Ser Leu Ala Ser Ala Asp Leu Val Met Gly Leu
     371
     372
                                   70
              Leu Val Val Pro Phe Gly Ala Thr Ile Val Val Trp Gly Arg Trp Glu
     374
     375
                                                    90
     377
              Tyr Gly Ser Phe Phe Cys Glu Leu Trp Thr Ser Val Asp Val Leu Cys
     378
                                                105
                                                                    110
     380
              Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Leu Asp Arg Tyr
     381
                                           120
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/988,745
DATE: 01/15/2002
TIME: 18:58:13

Input Set : N:\Crf3\RULE60\09988745.raw
Output Set: N:\CRF3\01152002\1988745.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:30 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:] L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9